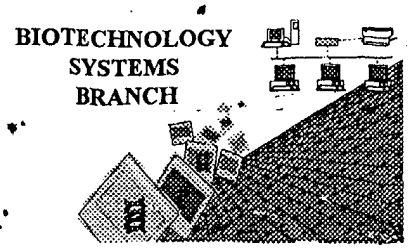

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/720,896
Source: IFW0
Date Processed by STIC: 12/16/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: **TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to (EFFECTIVE 12/01/03):** U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/720,896

DATE: 12/16/2003
TIME: 17:13:14

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12112003\J720896.raw

3 <110> APPLICANT: Solari, Roberto Celeste Ercole
4 Champion, Brian Robert
5 Ward, George Albert
7 <120> TITLE OF INVENTION: Conjugate of a Transport Protein and a Protein for Modulation
8 of Notch Signalling
10 <130> FILE REFERENCE: 674525-2007
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/720,896
C--> 13 <141> CURRENT FILING DATE: 2003-11-24
15 <150> PRIOR APPLICATION NUMBER: 2002-05-24
W--> 16 <151> PRIOR FILING DATE: PCT/GB02/02438
18 <150> PRIOR APPLICATION NUMBER: 2001-05-25
W--> 19 <151> PRIOR FILING DATE: GB 0112818.0
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 29
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial sequence
W--> 29 <220> FEATURE:
W--> 30 <221> NAME/KEY: PCR primer for amplifying HES1 promoter from mouse genomic DNA
W--> 32 <223> OTHER INFORMATION:
W--> 32 <400> 1
33 ggggtaccct caggcgcgcg ccattggcc 29
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 29
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial sequence
41 <220> FEATURE:
W--> 42 <221> NAME/KEY: PCR primer for amplifying HES1 promoter from mouse genomic DNA
W--> 44 <223> OTHER INFORMATION:
W--> 44 <400> 2
45 gaagatctgc ttacgtcctt ttacttgac 29
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 26
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial sequence
W--> 52 <220> FEATURE:
W--> 53 <221> NAME/KEY: Adenovirus major late promoter TATA-box motif with BglII and
W--> 54 HindIII cohesive ends
W--> 56 <223> OTHER INFORMATION:
W--> 56 <400> 3
57 gatctggggg gctataaaag ggggta 26
60 <210> SEQ ID NO: 4

Does Not Comply
Corrected Diskette Needed
(pg. 1-3)
A response for section <223 is mandatory, if Artificial sequence/UNKnown/ on Genus/ Species.

Please Remove, NOT Needed.

please move <221> Response to <223> section. Please see pg. 6 For error explanation.

Please Remove, Not Needed.

please move <221> Response to <223> section. Please see pg. 6 For error explanation.

Please Remove, Not Needed.

Please move <221> Response to <223> section. Please see pg. 6 For error explanation.

RAW SEQUENCE LISTING DATE: 12/16/2003
PATENT APPLICATION: US/10/720,896 TIME: 17:13:14

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12112003\J720896.raw

61 <211> LENGTH: 26
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial sequence
W--> 64 <220> FEATURE: please remove, not needed.
W--> 65 <221> NAME/KEY: Adenovirus major late promoter TATA-box motif with BglII and
W--> 66 HindIII cohesive ends
W--> 68 <223> OTHER INFORMATION: move to
W--> 68 <400> 4 same error
69 acccccccgat attttccccc attcga 26
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 61
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial sequence
W--> 76 <220> FEATURE: please remove, not needed.
W--> 77 <221> NAME/KEY: CBF-1 promoter tetramer with XhoI and BglII cohesive ends
W--> 79 <223> OTHER INFORMATION: move to
W--> 79 <400> 5 same error
80 tcgagaccgt gggaacttaa ccgtgggaac ttaaccgtgg gaacttaacc gtgggaactt 60
82 a 61
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 61
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial sequence
W--> 89 <220> FEATURE: please remove, not needed.
W--> 90 <221> NAME/KEY: CBF-1 promoter tetramer with XhoI and BglII cohesive ends
W--> 92 <223> OTHER INFORMATION: move to
W--> 92 <400> 6 same error
93 ctggcaccct tgaattggca cccttgaatt ggcacccttg aattggcacc cttgaatcta 60
95 g 61
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 39
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial sequence
W--> 102 <220> FEATURE: please remove, not needed.
W--> 103 <221> NAME/KEY: PCR amplimer for generating a truncated fragment of human
W--> 104 Notch1 cDNA
W--> 106 <223> OTHER INFORMATION: move to
W--> 106 <400> 7 same error
107 aaaggatcca ccatggcacg caagcgccgg cgcagtcat 39
110 <210> SEQ ID NO: 8
111 <211> LENGTH: 31
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial sequence
W--> 114 <220> FEATURE: please remove, not needed.
W--> 115 <221> NAME/KEY: PCR amplimer for generating a truncated fragment of human
W--> 116 Notch1 cDNA
W--> 118 <223> OTHER INFORMATION: move to
W--> 118 <400> 8 same error
119 gcgcctcgag ttagtccacg ggcgagagca t 31

RAW SEQUENCE LISTING DATE: 12/16/2003
PATENT APPLICATION: US/10/720,896 TIME: 17:13:14

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12112003\J720896.raw

```
     122 <210> SEQ ID NO: 9
     123 <211> LENGTH: 91
     124 <212> TYPE: DNA
     125 <213> ORGANISM: Artificial sequence
W--> 126 <220> FEATURE:
W--> 127 <221> NAME/KEY: Oligo annealed to the NIC2202 sequence to remove the stop
W--> 128       codon from theNIC2202 fragment of human Notch1 cDNA
W--> 130 <223> OTHER INFORMATION:
W--> 130 <400> 9
     131 cctggcctgt ggaagcaagg aggccaagga cctcaaggca cggaggaaga agtcccagga      60
     133 tggcaagggc tgcctgctgg acggcggccg c                                    91
     136 <210> SEQ ID NO: 10
     137 <211> LENGTH: 95
     138 <212> TYPE: DNA
     139 <213> ORGANISM: Artificial sequence
     141 <220> FEATURE:
W--> 142 <221> NAME/KEY: Oligo annealed to the NIC2202 sequence to remove the stop
W--> 143       codon from theNIC2202 fragment of human Notch1 cDNA
W--> 145 <223> OTHER INFORMATION:
W--> 145 <400> 10
     146 ggaccggaca ccttcgttcc tccggttcct ggagttccgt gcctccttct tcagggtcct      60
     148 accgttcccg acggacgacc tgccgccggc gagct                                95
     151 <210> SEQ ID NO: 11
     152 <211> LENGTH: 2556
     153 <212> TYPE: PRT
     154 <213> ORGANISM: Homo sapiens
     156 <220> FEATURE:
     157 <221> NAME/KEY: MISC_FEATURE
     158 <222> LOCATION: (891)..(892)
     159 <223> OTHER INFORMATION: x = any amino acid
     162 <400> SEQUENCE: 11
     164 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
     165 1               5                  10                  15
     168 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
     169             20                  25                  30
     172 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
     173         35                  40                  45
     176 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
     177     50                  55                  60
     180 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
     181 65                  70                  75                  80
     184 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
     185                 85                  90                  95
     188 Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
     189             100                 105                 110
     192 Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
     193         115                 120                 125
     196 Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys
     197     130                 135                 140
```

Please remove, not needed.

Please remove, not needed.

move to

same error

move to

same error

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING DATE: 12/16/2003
PATENT APPLICATION: **US/10/720,896** TIME: 17:13:14

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12112003\J720896.raw**

```
200 Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala
201 145                 150                 155                 160
204 Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg
205                 165                 170                 175
208 Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly
209             180                 185                 190
212 Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala
213         195                 200                 205
216 Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro
217     210                 215                 220
220 Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr
221 225                 230                 235                 240
224 His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu
225                 245                 250                 255
228 Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys
229             260                 265                 270
232 Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr
233         275                 280                 285
236 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn
237     290                 295                 300
240 Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn
241 305                 310                 315                 320
244 Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile
245                 325                 330                 335
248 Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp
249             340                 345                 350
252 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
253         355                 360                 365
256 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
257     370                 375                 380
260 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
261 385                 390                 395                 400
264 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
265                 405                 410                 415
268 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
269             420                 425                 430
272 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
273         435                 440                 445
276 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
277     450                 455                 460
280 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
281 465                 470                 475                 480
284 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
285                 485                 490                 495
288 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
289             500                 505                 510
292 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
293         515                 520                 525
296 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu
```

RAW SEQUENCE LISTING DATE: 12/16/2003
PATENT APPLICATION: **US/10/720,896** TIME: 17:13:14

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12112003\J720896.raw**

```
297     530                 535                 540
300 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly
301 545                 550                 555                 560
304 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His
305                 565                 570                 575
308 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg
309             580                 585                 590
312 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser
313         595                 600                 605
316 Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala
317     610                 615                 620
320 Tyr Leu Cys Phe Cys Leu Lys Gly Thr Thr Gly Pro Asn Cys Glu Ile
321 625                 630                 635                 640
324 Asn Leu Asp Asp Cys Ala Ser Ser Pro Cys Asp Ser Gly Thr Cys Leu
325                 645                 650                 655
328 Asp Lys Ile Asp Gly Tyr Glu Cys Ala Cys Glu Pro Gly Tyr Thr Gly
329             660                 665                 670
332 Ser Met Cys Asn Ser Asn Ile Asp Glu Cys Ala Gly Asn Pro Cys His
333         675                 680                 685
336 Asn Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly Phe Thr Cys Arg Cys
337     690                 695                 700
340 Pro Glu Gly Tyr His Asp Pro Thr Cys Leu Ser Glu Val Asn Glu Cys
341 705                 710                 715                 720
344 Asn Ser Asn Pro Cys Val His Gly Ala Cys Arg Asp Ser Leu Asn Gly
345                 725                 730                 735
348 Tyr Lys Cys Asp Cys Asp Pro Gly Trp Ser Gly Thr Asn Cys Asp Ile
349             740                 745                 750
352 Asn Asn Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Gly Thr Cys
353         755                 760                 765
356 Lys Asp Met Thr Ser Gly Ile Val Cys Thr Cys Arg Glu Gly Phe Ser
357     770                 775                 780
360 Gly Pro Asn Cys Gln Thr Asn Ile Asn Glu Cys Ala Ser Asn Pro Cys
361 785                 790                 795                 800
364 Leu Asn Lys Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn
365                 805                 810                 815
368 Cys Leu Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro
369             820                 825                 830
372 Cys Ala Pro Ser Pro Cys Arg Asn Gly Gly Glu Cys Arg Gln Ser Glu
373         835                 840                 845
376 Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly
377     850                 855                 860
380 Gln Thr Cys Glu Val Asp Ile Asn Glu Cys Val Leu Ser Pro Cys Arg
381 865                 870                 875                 880
W--> 384 His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys
385                 885                 890                 895
388 Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys
389             900                 905                 910
392 Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn
393         915                 920                 925
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/16/2003
PATENT APPLICATION: US/10/720,896 TIME: 17:13:15

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12112003\J720896.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 891

Error Explanation:

Use of <220> Feature(NEW RULES):
Sequence(s) __ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or"Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10

VERIFICATION SUMMARY DATE: 12/16/2003
PATENT APPLICATION: **US/10/720,896** TIME: 17:13:15

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12112003\J720896.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:29 M:283 W: Missing Blank Line separator, <220> field identifier
L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial sequence
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:32
L:42 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:44 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial sequence
L:44 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:44
L:52 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:54 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:3
L:56 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial sequence
L:56 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:56
L:64 M:283 W: Missing Blank Line separator, <220> field identifier
L:65 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:66 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4
L:68 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial sequence
L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:68
L:76 M:283 W: Missing Blank Line separator, <220> field identifier
L:77 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:79 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial sequence
L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:79
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:92 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial sequence
L:92 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:92
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:103 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:104 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:7
L:106 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial sequence
L:106 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:106
L:114 M:283 W: Missing Blank Line separator, <220> field identifier
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:116 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:8
L:118 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial sequence
L:118 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:118
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:128 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:9
L:130 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial sequence
L:130 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:130

```
L:142 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:143 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:10
L:145 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial sequence
L:145 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:145
```

VERIFICATION SUMMARY DATE: 12/16/2003
PATENT APPLICATION: **US/10/720,896** TIME: 17:13:15

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12112003\J720896.raw**

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:880